

Appendix A

ALIGNMENTS

RESULT 1

US-08-825-556A-2  
; Sequence 2, Application US/08825556A  
; Patent No. 5910431  
; GENERAL INFORMATION:  
; APPLICANT: NI, Jian  
; APPLICANT: Gentz, Reiner L.  
; APPLICANT: Su, Jeffrey Y.  
; APPLICANT: Li, Haodong  
; TITLE OF INVENTION: Chemokine Alpha 2  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-2934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/825,556A  
; FILING DATE: 19-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/013,653  
; FILING DATE: 19-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0850001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-825-556A-2

Query Match 99.1%; Score 582; DB 2; Length 111;  
Best Local Similarity 99.1%; Pred. No. 9.3e-64;  
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLLPRRAPPVSMRLAAALLLLLLLALYARVDGSKCKSRGPKIRYSDVKKLEMPKY 60

DB 1 MSLLPRRAPPVSMRLAAALLLLLLLALYARVDGSKCKSRGPKIRYSDVKKLEMPKY 60  
QY 61 PCEEEKWLIITTKSVSYRGQEHCLHPKLOSTKRFIKWYNANNEKRRVYEE 111  
DB 61 PCEEEKWLIITTKSVSYRGQEHCLHPKLOSTKRFIKWYNANNEKRRVYEE 111

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OM protein - protein search, using sw model

Run On: October 23, 2002, 12:00:08 ; Search time 12.3333 Seconds  
(without alignments)  
219,830 Million cell updates/sec

Title: US-09-816-920-2  
Perfect score: 587  
Sequence: 1 MSLLPRRAPPVSMRLAAAL.....TKRFIKWYNANNEKRRVYEE 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	582	99.1	111 2	US-08-825-556A-2